Abstract

Described is a method for methylation detection in a DNA sample. An isolated genomic DNA sample is treated in a manner capable of distinguishing methylated from unmethylated cytosine bases. The pretreated DNA is amplified using at least one oligonucleotide primer, a polymerase and a set of nucleotides of which at least one is labeled with a first type of label. A sequence-specific oligonucleotide probe, marked with a second type of label, hybridizes to the amplification product and a FRET reaction occurs if a labeled oligonucleotide is present in close proximity in the amplification product. The method determines the level of methylation of a sample by measuring the extent of fluorescence resonance energy transfer (FRET) between the donor and acceptor fluorophore.